

SEQUENCE LISTINGS

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: COOPERATIVE RESEARCH CENTRE FOR TROPICAL PLANT
PATHOLOGY
(B) STREET: The University of Queensland
(C) CITY: St Lucia
(D) STATE: Queensland
(E) COUNTRY: Australia
(F) POSTAL CODE (ZIP): 4067

(ii) TITLE OF INVENTION: Antimicrobial Protein

(iii) NUMBER OF SEQUENCES: 28

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Macadamia integrifolia
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Ile Asn Thr Ser Asn Leu Cys Ser Leu Leu Phe Leu Leu Ser
1 5 10 15

Leu Phe Leu Leu Ser Thr Thr Val Ser Leu Ala Glu Ser Glu Phe Asp
20 25 30

Arg Gln Glu Tyr Glu Glu Cys Lys Arg Gln Cys Met Gln Leu Glu Thr
35 40 45

Ser Gly Gln Met Arg Arg Cys Val Ser Gln Cys Asp Lys Arg Phe Glu
50 55 60

Glu Asp Ile Asp Trp Ser Lys Tyr Asp Asn Gln Glu Asp Pro Gln Thr

35

| | | | | | | | |
|----|---|-----|----|-----|----|-----|-----|
| | 65 | | 70 | | 75 | | 80 |
| | Glu Cys Gln Gln Cys Gln Arg Arg Cys Arg Gln Gln Glu Ser Gly Pro | 85 | | 90 | | 95 | |
| 5 | Arg Gln Gln Gln Tyr Cys Gln Arg Arg Cys Lys Glu Ile Cys Glu Glu | 100 | | 105 | | 110 | |
| | Glu Glu Glu Tyr Asn Arg Gln Arg Asp Pro Gln Gln Gln Tyr Glu Gln | 115 | | 120 | | 125 | |
| 10 | Cys Gln Lys His Cys Gln Arg Arg Glu Thr Glu Pro Arg His Met Gln | 130 | | 135 | | 140 | |
| | Thr Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu Lys Glu Lys Arg Lys | 145 | | 150 | | 155 | 160 |
| | Gln Gln Lys Arg Tyr Glu Glu Gln Gln Arg Glu Asp Glu Glu Lys Tyr | 165 | | 170 | | 175 | |
| 20 | Glu Glu Arg Met Lys Glu Glu Asp Asn Lys Arg Asp Pro Gln Gln Arg | 180 | | 185 | | 190 | |
| | Glu Tyr Glu Asp Cys Arg Arg Arg Cys Glu Gln Gln Glu Pro Arg Gln | 195 | | 200 | | 205 | |
| | Gln His Gln Cys Gln Leu Arg Cys Arg Glu Gln Gln Arg Gln His Gly | 210 | | 215 | | 220 | |
| 30 | Arg Gly Gly Asp Met Met Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr | 225 | | 230 | | 235 | 240 |
| | Glu Glu Gly Glu Glu Glu Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu | 245 | | 250 | | 255 | |
| 35 | Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val | 260 | | 265 | | 270 | |
| | Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn | 275 | | 280 | | 285 | |
| 40 | Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro | 290 | | 295 | | 300 | |
| | Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Ile Gly Gly Arg Gly | 305 | | 310 | | 315 | 320 |
| | Ala Leu Lys Met Ile His His Asp Asn Arg Glu Ser Tyr Asn Leu Glu | 325 | | 330 | | 335 | |
| 50 | Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile | 340 | | 345 | | 350 | |
| | Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr | 355 | | 360 | | 365 | |
| 55 | | | | | | | |

66250:TESFEED

36

Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 370 375 380
 5 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 385 390 395 400
 Ala Leu Asn Thr Gln Thr Glu Lys Leu Arg Gly Val Phe Gly Gln Gln
 405 410 415
 10 Arg Glu Gly Val Ile Ile Arg Ala Ser Gln Glu Gln Ile Arg Glu Leu
 420 425 430
 Thr Arg Asp Asp Ser Glu Ser Arg His Trp His Ile Arg Arg Gly Gly
 435 440 445
 15 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460
 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 465 470 475 480
 Gln Leu Gln Asp Met Asp Leu Ser Val Phe Ile Ala Asn Val Thr Gln
 485 490 495
 25 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 500 505 510
 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu
 515 520 525
 30 Ser Gly Arg His Gly Gly Arg Gly Gly Gly Lys Arg His Glu Glu Glu
 530 535 540
 Glu Asp Val His Tyr Glu Gln Val Arg Ala Arg Leu Ser Lys Arg Glu
 545 550 555 560
 Ala Ile Val Val Leu Ala Gly His Pro Val Val Phe Val Ser Ser Gly
 565 570 575
 40 Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
 580 585 590
 His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
 595 600 605
 45 Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
 610 615 620
 Glu Glu Ser Phe Asn Ser Gln Asp Gln Ser Ile Phe Phe Pro Gly Pro
 625 630 635 640
 Arg Gln His Gln Gln Gln Ser Pro Arg Ser Thr Lys Gln Gln Gln Pro
 645 650 655
 55 Leu Val Ser Ile Leu Asp Phe Val Gly Phe
 660 665

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Macadamia integrifolia*
15 (F) TISSUE TYPE: Seeds

- (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:1..85
- 20

- (x) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:86..1999
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTTTCACT CTCCTTCTG 60

30 TCTACGACAG TGTCTCTTGC TGAAAGTGAA TTTGACAGGC AGGAATATGA GGAGTGCAAA 120

CGGCAATGCA TGCAGTTGGA GACATCAGGC CAGATGCGTC GGTGTGTGAG TCAGTGCGAT 180

AAGAGATTTG AAGAGGATAT AGATTGGTCT AAGTATGATA ACCAAGAGGA TCCTCAGACG 240

35 GAATGCCAAC AATGCCAGAG GCGATGCAGG CAGCAGGAGA GTGGCCCACG TCAGCAACAA 300

TACTGCCAAC GACGCTGCAA GGAAATATGT GAAGAAGAAG AAGAATATAA CCGACAACGT 360

40 GATCCACAGC AGCAATACGA GCAATGTCAG AAGCACTGCC AACGGCGCGA GACAGAGCCA 420

CGTCACATGC AAACATGTCA ACAACGCTGC GAGAGGAGAT ATGAAAAGGA GAAACGTAAG 480

CAACAAAAGA GATATGAAGA GCAACAACGT GAAGACGAAG AGAAATATGA AGAGCGAATG 540

45 AAGGAAGAAG ATAACAAACG CGATCCACAA CAAAGAGAGT ACGAAGACTG CCGGAGGCGC 600

TGCGAACAAC AGGAGCCACG TCAGCAGCAC CAGTGCCAGC TAAGATGCCG AGAGCAGCAG 660

50 AGGCAACACG GCCGAGGTGG CGATATGATG AACCTCAGA GGGGAGGCAG CGGCAGATAC 720

GAGGAGGGAG AAGAGGAGCA AAGCGACAAC CCCTACTACT TCGACGAACG AAGCTTAAGT 780

ACAAGGTTCA GGACCGAGGA AGGCCACATC TCAGTTCTGG AGAACTTCTA TGGTAGATCC 840

55 AAGCTTCTAC GCGCACTAAA AACTATCGC TTGGTGCTCC TCGAGGCTAA CCCCACGCC 900

TTCTGCTCC CTACCCACTT GGATGCAGAT GCCATTCTCT TGGTCATAGG AGGGAGAGGA 960
5 GCCCTCAAAA TGATCCACCA CGACAACAGA GAATCCTACA ACCTCGAGTG TGGAGACGTA 1020
ATCAGAATCC CAGCTGGAAC CACATTCTAC TTAATCAACC GAGACAACAA CGAGAGGCTC 1080
CACATAGCCA AGTTCTTACA GACCATATCC ACTCCTGGCC AATACAAGGA ATTCTTCCCA 1140
10 GCTGGAGGCC AAAACCCAGA GCCGTACCTC AGTACCTTCA GCAAAGAGAT TCTCGAGGCT 1200
GCGCTCAACA CACAAACAGA GAAGCTGCGT GGGGTGTTTG GACAGCAAAG GGAGGGAGTG 1260
ATAATTAGGG CGTCACAGGA GCAGATCAGG GAGTTGACTC GAGATGACTC AGAGTCACGA 1320
15 CACTGGCATA TAAGGAGAGG TGGTGAATCA AGCAGGGGAC CTTACAATCT GTTCAACAAA 1380
AGGCCACTGT ACTCCAACAA ATACGGTCAA GCCTACGAAG TCAAACCTGA GGACTACAGG 1440
20 CAACTCCAAG ACATGGACTT ATCGGTTTTT ATAGCCAACG TCACCCAGGG ATCCATGATG 1500
GGTCCCTTCT TCAACACTAG GTCTACAAAG GTGGTAGTGG TGGCTAGTGG AGAGGCAGAT 1560
GTGGAAATGG CATGCCCTCA CTTGTCGGA AGACACGGCG GCCGCGGTGG AGGAAAAAGG 1620
25 CATGAGGAGG AAGAGGATGT GCACTATGAG CAGGTTAGAG CACGTTTGTC GAAGAGAGAG 1680
GCCATTGTTG TTCTGGCAGG TCATCCCGTC GTCTTCGTTT CATCCGGAAA CGAGAACCTG 1740
30 CTGCTTTTTT CATTGTGAAT CAATGCCCAA AACAACCACG AGAACTTCCT CGCGGGGAGA 1800
GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA 1860
AGGAAAGAGG TAGAAGAGTC ATTTAACAGC CAGGACCAGT CTATCTTCTT TCCTGGGCCC 1920
35 AGGCAGCACC AGCAACAGTC GCCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT 1980
CTGGAATTCT TTGGCTTCTA AAGTTCCACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG 2040
40 TAGCTCCTAG CTCGGTGTAT GAGAGTGGTA AGAGACTAAG ACGCTAAATC CCTAAGTAAC 2100
TAACCTGGCG AGCTTGCGTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTTAAAAAAA 2160
45 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO: 3:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Macadamia integrifolia*
 (F) TISSUE TYPE: Seeds

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION:1..28

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION:29..666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Asn | Thr | Ser | Asn | Leu | Cys | Ser | Leu | Leu | Phe | Leu | Leu | Ser | 1 | 5 | 10 | 15 |
| Leu | Phe | Leu | Leu | Ser | Thr | Thr | Val | Ser | Leu | Ala | Glu | Ser | Glu | Phe | Asp | 20 | 25 | 30 | |
| Arg | Gln | Glu | Tyr | Glu | Glu | Cys | Lys | Arg | Gln | Cys | Met | Gln | Leu | Glu | Thr | 35 | 40 | 45 | |
| Ser | Gly | Gln | Met | Arg | Arg | Cys | Val | Ser | Gln | Cys | Asp | Lys | Arg | Phe | Glu | 50 | 55 | 60 | |
| Glu | Asp | Ile | Asp | Trp | Ser | Lys | Tyr | Asp | Asn | Gln | Asp | Asp | Pro | Gln | Thr | 65 | 70 | 75 | 80 |
| Asp | Cys | Gln | Gln | Cys | Gln | Arg | Arg | Cys | Arg | Gln | Gln | Glu | Ser | Gly | Pro | 85 | 90 | 95 | |
| Arg | Gln | Gln | Gln | Tyr | Cys | Gln | Arg | Arg | Cys | Lys | Glu | Ile | Cys | Glu | Glu | 100 | 105 | 110 | |
| Glu | Glu | Glu | Tyr | Asn | Arg | Gln | Arg | Asp | Pro | Gln | Gln | Gln | Tyr | Glu | Gln | 115 | 120 | 125 | |
| Cys | Gln | Glu | Arg | Cys | Gln | Arg | His | Glu | Thr | Glu | Pro | Arg | His | Met | Gln | 130 | 135 | 140 | |
| Thr | Cys | Gln | Gln | Arg | Cys | Glu | Arg | Arg | Tyr | Glu | Lys | Glu | Lys | Arg | Lys | 145 | 150 | 155 | 160 |
| Gln | Gln | Lys | Arg | Tyr | Glu | Glu | Gln | Gln | Arg | Glu | Asp | Glu | Glu | Lys | Tyr | 165 | 170 | 175 | |
| Glu | Glu | Arg | Met | Lys | Glu | Glu | Asp | Asn | Lys | Arg | Asp | Pro | Gln | Gln | Arg | 180 | 185 | 190 | |
| Glu | Tyr | Glu | Asp | Cys | Arg | Arg | Arg | Cys | Glu | Gln | Gln | Glu | Pro | Arg | Gln | 195 | 200 | 205 | |
| Gln | Tyr | Gln | Cys | Gln | Arg | Arg | Cys | Arg | Glu | Gln | Gln | Arg | Gln | His | Gly | 210 | 215 | 220 | |

Arg Gly Gly Asp Leu Ile Asn Pro Gln Arg Gly Gly Ser Gly Arg Tyr
 225 230 235 240
 5 Glu Glu Gly Glu Glu Lys Gln Ser Asp Asn Pro Tyr Tyr Phe Asp Glu
 245 250 255
 Arg Ser Leu Ser Thr Arg Phe Arg Thr Glu Glu Gly His Ile Ser Val
 260 265 270
 10 Leu Glu Asn Phe Tyr Gly Arg Ser Lys Leu Leu Arg Ala Leu Lys Asn
 275 280 285
 Tyr Arg Leu Val Leu Leu Glu Ala Asn Pro Asn Ala Phe Val Leu Pro
 290 295 300
 15 Thr His Leu Asp Ala Asp Ala Ile Leu Leu Val Thr Gly Gly Arg Gly
 305 310 315 320
 20 Ala Leu Lys Met Ile His Arg Asp Asn Arg Glu Ser Tyr Asn Leu Glu
 325 330 335
 Cys Gly Asp Val Ile Arg Ile Pro Ala Gly Thr Thr Phe Tyr Leu Ile
 340 345 350
 25 Asn Arg Asp Asn Asn Glu Arg Leu His Ile Ala Lys Phe Leu Gln Thr
 355 360 365
 Ile Ser Thr Pro Gly Gln Tyr Lys Glu Phe Phe Pro Ala Gly Gly Gln
 370 375 380
 30 Asn Pro Glu Pro Tyr Leu Ser Thr Phe Ser Lys Glu Ile Leu Glu Ala
 385 390 395 400
 35 Ala Leu Asn Thr Gln Ala Glu Arg Leu Arg Gly Val Leu Gly Gln Gln
 405 410 415
 Arg Glu Gly Val Ile Ile Ser Ala Ser Gln Glu Gln Ile Arg Glu Leu
 420 425 430
 40 Thr Arg Asp Asp Ser Glu Ser Arg Arg Trp His Ile Arg Arg Gly Gly
 435 440 445
 45 Glu Ser Ser Arg Gly Pro Tyr Asn Leu Phe Asn Lys Arg Pro Leu Tyr
 450 455 460
 Ser Asn Lys Tyr Gly Gln Ala Tyr Glu Val Lys Pro Glu Asp Tyr Arg
 465 470 475 480
 50 Gln Leu Gln Asp Met Asp Val Ser Val Phe Ile Ala Asn Ile Thr Gln
 485 490 495
 Gly Ser Met Met Gly Pro Phe Phe Asn Thr Arg Ser Thr Lys Val Val
 500 505 510
 55 Val Val Ala Ser Gly Glu Ala Asp Val Glu Met Ala Cys Pro His Leu

41

515

520

525

Ser Gly Arg His Gly Gly Arg Arg Gly Gly Lys Arg His Glu Glu Glu
530 535 540

Glu Asp Val His Tyr Glu Gln Val Lys Ala Arg Leu Ser Lys Arg Glu
545 550 555 560

Ala Ile Val Val Pro Val Gly His Pro Val Val Phe Val Ser Ser Gly
565 570 575

Asn Glu Asn Leu Leu Leu Phe Ala Phe Gly Ile Asn Ala Gln Asn Asn
580 585 590

His Glu Asn Phe Leu Ala Gly Arg Glu Arg Asn Val Leu Gln Gln Ile
595 600 605

Glu Pro Gln Ala Met Glu Leu Ala Phe Ala Ala Pro Arg Lys Glu Val
610 615 620

Glu Glu Leu Phe Asn Ser Gln Asp Glu Ser Ile Phe Phe Pro Gly Pro
625 630 635 640

Arg Gln His Gln Gln Gln Ser Ser Arg Ser Thr Lys Gln Gln Gln Pro
645 650 655

Leu Val Ser Ile Leu Asp Phe Val Gly Phe
660 665

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macadamia integrifolia*
- (F) TISSUE TYPE: Seeds

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION:1..86

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION:87..1999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGGCGATCA ATACATCAAA TTTATGTTCT CTTCTCTTTC TCCTTTCCT CTCCTTCTG

60

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|------------|------|
| | TCAACGACAG | TGTCTCTTGC | TGAAAGTGAA | TTTGACAGGC | AGGAATATGA | GGAGTGCAAA | 120 |
| 5 | CGGCAATGCA | TGCAGTTGGA | GACATCAGGC | CAGATGCGTC | GGTGTGTGAG | TCAGTGCGAT | 180 |
| | AAGAGATTTG | AAGAGGATAT | AGATTGGTCT | AAGTATGATA | ACCAAGACGA | TCCTCAGACG | 240 |
| | GATTGCCAAC | AATGCCAGAG | GCGATGCAGG | CAGCAGGAGA | GTGGCCCACG | TCAGCAACAA | 300 |
| 10 | TACTGCCAAC | GACGCTGCAA | GGAAATATGT | GAAGAAGAAG | AAGAATATAA | CCGACAACGT | 360 |
| | GATCCACAGC | AGCAATACGA | GCAATGTCAG | GAGCGCTGCC | AACGGCACGA | GACAGAGCCA | 420 |
| 15 | CGTCACATGC | AAACATGTCA | ACAACGCTGC | GAGAGGAGAT | ATGAAAAGGA | GAAACGTAAG | 480 |
| | CAACAAAAGA | GATATGAAGA | GCAACAACGT | GAAGACGAAG | AGAAATATGA | AGAGCGAATG | 540 |
| | AAGGAAGAAG | ATAACAAACG | CGATCCACAA | CAAAGAGAGT | ACGAAGACTG | CCGGAGGCGC | 600 |
| 20 | TGCGAACAAAC | AGGAGCCACG | TCAGCAGTAC | CAGTGCCAGC | GAAGATGCCG | AGAGCAGCAG | 660 |
| | AGGCAACACG | GCCGAGGTGG | TGATTTGATT | AACCCTCAGA | GGGGAGGCAG | CGGCAGATAC | 720 |
| 25 | GAGGAGGGAG | AAGAGAAGCA | AAGCGACAAC | CCCTACTACT | TCGACGAACG | AAGCTTAAGT | 780 |
| | ACAAGGTTCA | GGACCGAGGA | AGGCCACATC | TCAGTTCTGG | AGAACTTCTA | TGGTAGATCC | 840 |
| | AAGCTTCTAC | GCGCACTAAA | AAACTATCGC | TTGGTGCTCC | TCGAGGCTAA | CCCCAACGCC | 900 |
| 30 | TTCGTGCTCC | CTACCCACTT | GGACGCAGAT | GCCATTCTCT | TGGTCACCGG | AGGGAGAGGA | 960 |
| | GCCCTCAAAA | TGATCCACCG | TGACAACAGA | GAATCCTACA | ACCTCGAGTG | TGGAGACGTA | 1020 |
| 35 | ATCAGAATCC | CAGCTGGAAC | CACATTCTAC | TTAATCAACC | GAGACAACAA | CGAGAGGCTC | 1080 |
| | CACATAGCCA | AGTTCTTACA | GACCATATCC | ACTCCTGGCC | AATACAAGGA | ATTCTTCCCA | 1140 |
| | GCTGGAGGCC | AAAACCCAGA | GCCGTACCTC | AGTACCTTCA | GCAAAGAGAT | TCTCGAGGCT | 1200 |
| 40 | GCGCTCAACA | CACAAGCAGA | GAGGCTGCGT | GGGGTGCTTG | GACAGCAAAG | GGAGGGAGTG | 1260 |
| | ATAATTAGTG | CGTCACAGGA | GCAGATCAGG | GAGTTGACTC | GAGATGACTC | AGAGTCACGA | 1320 |
| 45 | CGCTGGCATA | TAAGGAGAGG | TGGTGAATCA | AGCAGGGGAC | CTTACAATCT | GTTCAACAAA | 1380 |
| | AGGCCACTGT | ACTCCAACAA | ATACGGTCAA | GCCTACGAAG | TCAAACCTGA | GGACTACAGG | 1440 |
| | CAACTCCAAG | ACATGGACGT | ATCGGTTTTT | ATAGCCAACA | TCACCCAGGG | ATCCATGATG | 1500 |
| 50 | GGTCCCTTCT | TCAACACTAG | GTCTACAAAG | GTGGTAGTGG | TGGCTAGTGG | AGAGGCAGAT | 1560 |
| | GTGGAAATGG | CATGCCCTCA | CTTGTCGGGA | AGACACGGCG | GCCGCCGTGG | AGGGAAAAGG | 1620 |
| 55 | CATGAGGAGG | AAGAGGATGT | GCACTATGAG | CAGGTTAAAG | CACGTTTGTC | GAAGAGAGAG | 1680 |
| | GCCATTGTTG | TTCCGGTAGG | TCATCCCGTC | GTCTTCGTTT | CATCCGAAA | CGAGAACCTG | 1740 |

CTGCTTTTTG CATTGTGAAT CAATGCCCAA AACAACCACG AGAACTTCCT CGCGGGGAGA 1800
5 GAGAGGAACG TGCTGCAGCA GATAGAGCCA CAGGCAATGG AGCTAGCGTT TGCCGCTCCA 1860
AGGAAAGAGG TAGAAGAGTT ATTTAACAGC CAGGACGAGT CTATCTTCTT TCCTGGGCCC 1920
AGGCAGCACC AGCAACAGTC TTCCCGCTCC ACCAAGCAAC AACAGCCTCT CGTCTCCATT 1980
10 CTGGACTTCG TTGGCTTCTA AAGTTCTACA AAAAAGAGTG TGTTATGTAG TATAGGTTAG 2040
TAGCTCCTAG CTCGGTGTAT GCGAGTGGTA AGAGACCAAG ACGCTAAATC CCTAAGTAAC 2100
TAACCTGGCG AGCTTGCGTG TATGCAAATA AAGAGGAACA GCTTTCCAAC TTAAAAAAA 2160
15 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macadamia integrifolia*
(F) TISSUE TYPE: Seeds

(ix) FEATURE:

- (A) NAME/KEY: partial mat_peptide
(B) LOCATION:1..625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

40 Gln Cys Met Gln Leu Glu Thr Ser Gly Gln Met Arg Arg Cys Val Ser
1 5 10 15
Gln Cys Asp Lys Arg Phe Glu Glu Asp Ile Asp Trp Ser Lys Tyr Asp
20 25 30
45 Asn Gln Glu Asp Pro Gln Thr Glu Cys Gln Gln Cys Gln Arg Arg Cys
35 40 45
Arg Gln Gln Glu Ser Asp Pro Arg Gln Gln Gln Tyr Cys Gln Arg Arg
50 55 60
Cys Lys Glu Ile Cys Glu Glu Glu Glu Tyr Asn Arg Gln Arg Asp
65 70 75 80
55 Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu
85 90 95

44

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Thr | Glu | Pro | Arg | His | Met | Gln | Ile | Cys | Gln | Gln | Arg | Cys | Glu | Arg | Arg | |
| | | | | | | 100 | | | | 105 | | | | | 110 | | |
| 5 | Tyr | Glu | Lys | Glu | Lys | Arg | Lys | Gln | Gln | Lys | Arg | Tyr | Glu | Glu | Gln | Gln | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| | Arg | Glu | Asp | Glu | Glu | Lys | Tyr | Glu | Glu | Arg | Met | Lys | Glu | Gly | Asp | Asn | |
| | | | 130 | | | | 135 | | | | | 140 | | | | | |
| 10 | Lys | Arg | Asp | Pro | Gln | Gln | Arg | Glu | Tyr | Glu | Asp | Cys | Arg | Arg | His | Cys | |
| | | | | | | 150 | | | | | 155 | | | | | 160 | |
| | Glu | Gln | Gln | Glu | Pro | Arg | Leu | Gln | Tyr | Gln | Cys | Gln | Arg | Arg | Cys | Gln | |
| 15 | | | | | 170 | | | | | 175 | | | | | 180 | | |
| | Glu | Gln | Gln | Arg | Gln | His | Gly | Arg | Gly | Gly | Asp | Leu | Met | Asn | Pro | Gln | |
| | | | | 185 | | | | | 190 | | | | | 195 | | | |
| 20 | Arg | Gly | Gly | Ser | Gly | Arg | Tyr | Glu | Glu | Gly | Glu | Glu | Lys | Gln | Ser | Asp | |
| | | | 200 | | | | | 205 | | | | | | 210 | | | |
| | Asn | Pro | Tyr | Tyr | Phe | Asp | Glu | Arg | Ser | Leu | Ser | Thr | Arg | Phe | Arg | Thr | |
| | | | 215 | | | | 220 | | | | | 225 | | | | | |
| 25 | Glu | Glu | Gly | His | Ile | Ser | Val | Leu | Glu | Asn | Phe | Tyr | Gly | Arg | Ser | Lys | |
| | | | | | 235 | | | | | | 240 | | | | | 245 | |
| | Leu | Leu | Arg | Ala | Leu | Lys | Asn | Tyr | Arg | Leu | Val | Leu | Leu | Glu | Ala | Asn | |
| 30 | | | | | 250 | | | | | 255 | | | | | 260 | | |
| | Pro | Asn | Ala | Phe | Val | Leu | Pro | Thr | His | Leu | Asp | Ala | Asp | Ala | Ile | Leu | |
| | | | | 265 | | | | 270 | | | | | | 275 | | | |
| 35 | Leu | Val | Ile | Gly | Gly | Arg | Gly | Ala | Leu | Lys | Met | Ile | His | Arg | Asp | Asn | |
| | | | 280 | | | | | 285 | | | | | 290 | | | | |
| | Arg | Glu | Ser | Tyr | Asn | Leu | Glu | Cys | Gly | Asp | Val | Ile | Arg | Ile | Pro | Ala | |
| | | | | | | 300 | | | | | | 305 | | | | | |
| 40 | Gly | Thr | Thr | Phe | Tyr | Leu | Ile | Asn | Arg | Asp | Asn | Asn | Glu | Arg | Leu | His | |
| | | | | | | 315 | | | | | 320 | | | | | 325 | |
| | Ile | Ala | Lys | Phe | Leu | Gln | Thr | Ile | Ser | Thr | Pro | Gly | Gln | Tyr | Lys | Glu | |
| 45 | | | | | 330 | | | | | 335 | | | | | 340 | | |
| | Phe | Phe | Pro | Ala | Gly | Gly | Gln | Asn | Pro | Glu | Pro | Tyr | Leu | Ser | Thr | Phe | |
| | | | | 345 | | | | 350 | | | | | | 355 | | | |
| 50 | Ser | Lys | Glu | Ile | Leu | Glu | Ala | Ala | Leu | Asn | Thr | Gln | Thr | Glu | Arg | Leu | |
| | | | 360 | | | | 365 | | | | | | 370 | | | | |
| | Arg | Gly | Val | Leu | Gly | Gln | Gln | Arg | Glu | Gly | Val | Ile | Ile | Arg | Ala | Ser | |
| | | | | | 375 | | 380 | | | | | 385 | | | | | |
| 55 | Gln | Glu | Gln | Ile | Arg | Glu | Leu | Thr | Arg | Asp | Asp | Ser | Glu | Ser | Arg | Arg | |
| | | | | | | 395 | | | | | 400 | | | | | 405 | |

Trp His Ile Arg Arg Gly Gly Glu Ser Ser Arg Gly Pro Tyr Asn Leu
410 415 420

5 Phe Asn Lys Arg Pro Leu Tyr Ser Asn Lys Tyr Gly Gln Ala Tyr Glu
 425 430 435

Val Lys Pro Glu Asp Tyr Arg Gln Leu Gln Asp Met Asp Val Ser Val
440 445 450

10

Phe Ile Ala Asn Ile Thr Gln Gly Ser Met Met Gly Pro Phe Phe Asn
455 460 470

15

Thr Arg Ser Thr Lys Val Val Val Val Ala Ser Gly Glu Ala Asp Val
480 485 490 500

Glu Met Ala Cys Pro His Leu Ser Gly Arg His Gly Gly Arg Gly Gly
505 510 515

20

Gly Lys Arg His Glu Glu Glu Glu Glu Val His Tyr Glu Gln Val Arg
520 525 530

Ala Arg Leu Ser Lys Arg Glu Ala Ile Val Val Leu Ala Gly His Pro
535 540 545

25

Val Val Phe Val Ser Ser Gly Asn Glu Asn Leu Leu Leu Phe Ala Phe
550 555 560

30

Gly Ile Asn Ala Gln Asn Asn His Glu Asn Phe Leu Ala Gly Arg Glu
565 570 575 580

Arg Asn Val Leu Gln Gln Ile Glu Pro Gln Ala Met Glu Leu Ala Phe
585 590 595

35

Ala Ala Ser Arg Lys Glu Val Glu Glu Leu Phe Asn Ser Gln Asp Glu
600 605 610

Ser Ile Phe Phe Pro Gly Pro Arg Gln His Gln Gln Gln Ser Pro Arg
615 620 625

40

Ser Thr Lys Gln Gln Gln Pro Leu Val Ser Ile Leu Asp Phe Val Gly
630 635 640
Phe

45 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Macadamia integrifolia*

(F) TISSUE TYPE: Seeds

(x) FEATURE:

(A) NAME/KEY: partial mat_peptide

(B) LOCATION:1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

| | | |
|----|--|------|
| 10 | CAATGCATGC AGTTAGAGAC ATCAGGCCAG ATGCGTCGGT GTGTGAGTCA GTGCGATAAG | 60 |
| | AGATTTGAAG AGGATATAGA TTGGTCTAAG TATGATAACC AAGAGGATCC TCAGACGGAA | 120 |
| | TGCCAACAAT GCCAGAGGCG ATGCAGGCAG CAGGAGAGTG ACCCACGTCA GCAACAATAC | 180 |
| 15 | TGCCAACGAC GCTGCAAGGA AATATGTGAA GAAGAAGAAG AATATAACCG ACAACGTGAT | 240 |
| | CCACAGCAGC AATACGAGCA ATGTCAGAAG CGCTGCCAAC GGCGCGAGAC AGAGCCACGT | 300 |
| 20 | CACATGCAAA TATGTCAACA ACGCTGCGAG AGGAGATATG AAAAGGAGAA ACGTAAGCAA | 360 |
| | CAAAAGAGAT ATGAAGAGCA ACAACGTGAA GACGAAGAGA AATATGAAGA GCGAATGAAG | 420 |
| | GAAGGAGATA ACAAACGCGA TCCACAACAA AGAGAGTACG AAGACTGCCG GCGGCACTGC | 480 |
| 25 | GAACAACAGG AGCCACGTCT GCAGTACCAG TGCCAGCGAA GATGCCAAGA GCAGCAGAGG | 540 |
| | CAACACGGCC GAGGTGGCGA TTTGATGAAC CCTCAGAGGG GAGGCAGCGG CAGATACGAG | 600 |
| | GAGGGAGAAG AGAAGCAAAG CGACAACCCC TACTACTTCG ACGAACGAAG CTTAAGTACA | 660 |
| 30 | AGGTTTCAGGA CCGAGGAAGG CCACATCTCA GTTCTGGAGA ACTTCTATGG TAGATCCAAG | 720 |
| | CTTCTACGCG CACTAAAAAA CTATCGCTTG GTGCTCCTCG AGGCTAACCC CAACGCCTTC | 780 |
| 35 | GTGCTCCCTA CCCACTTGGA TGCAGATGCC ATTCTCTTGG TCATCGGAGG GAGAGGAGCC | 840 |
| | CTCAAAATGA TCCACCGTGA CAACAGAGAA TCCTACAACC TCGAGTGTGG AGACGTAATC | 900 |
| | AGAATCCCAG CTGGAACCAC ATTCTACTTA ATCAACCGAG ACAACAACGA GAGGCTCCAC | 960 |
| 40 | ATAGCCAAGT TCTTACAGAC CATATCCACT CCTGGCCAAT ACAAGGAATT CTTCCCAGCT | 1020 |
| | GGAGGCCAAA ACCCAGAGCC GTACCTCAGT ACCTTCAGCA AAGAGATTCT CGAGGCTGCG | 1080 |
| 45 | CTCAACACAC AAACAGAGAG GCTGCGTGGG GTGCTTGGAC AGCAAAGGGA GGGAGTGATA | 1140 |
| | ATTAGGGCGT CACAGGAGCA GATCAGGGAG TTGACTCGAG ATGACTCAGA GTCACGACGC | 1200 |
| | TGGCATATAA GGAGAGGTGG TGAATCAAGC AGGGGACCTT ACAATCTGTT CAACAAAAGG | 1260 |
| 50 | CCACTGTACT CCAACAAATA CGGTCAAGCC TACGAAGTCA AACCTGAGGA CTACAGGCAA | 1320 |
| | CTCCAAGACA TGGACGTATC AGTTTTTCATA GCCAACATCA CCCAGGGATC CATGATGGGT | 1380 |
| 55 | CCCTTCTTCA AACTAGGTC TACAAAGGTG GTAGTGGTGG CTAGTGGAGA GGCAGATGTG | 1440 |

GAAATGGCAT GCCCTCACTT GTCGGGAAGA CACGGCGGCC GCGGTGGAGG GAAAAGGCAT 1500
 GAGGAGGAAG AGGAGGTGCA CTATGAGCAG GTTAGAGCAC GTTTGTCGAA GAGAGAGGCC 1560
 5 ATTGTTGTTC TGGCAGGTCA TCCCGTCGTC TTCGTTTCAT CCGGAAACGA AAACCTGCTG 1620
 CTTTTTGCAT TTGGAATCAA TGCCCAAAAC AACCACGAGA ACTTCCTCGC GGGGAGAGAG 1680
 10 AGGAACGTGC TGCAGCAGAT AGAGCCACAG GCAATGGAGC TAGCGTTTGC CGCTTCAAGG 1740
 AAAGAGGTAG AAGAGTTATT TAACAGCCAG GACGAGTCTA TCTTCTTTCC TGGGCCCAGG 1800
 CAGCACCAGC AACAGTCGCC CCGCTCCACC AAGCAACAAC AGCCTCTCGT CTCCATTCTG 1860
 15 GACTTCGTTG GCTTCTAAAG TTCTACAAAA AAGAGTGTGT TATGTAGTAT AGGTTAGTAG 1920
 CTCCTAGCTC GGTGTATGAG AGTGGTAAGA GACTAAGACG CTAAATCCCT AAGTAACTAA 1980
 20 CCTGGCGAGC TTGCGTGTAT GCAAATAAAG AGGAACAGCT TTCCAACCTT AGAAAGCTCT 2040
 TTTTTTTTTT TTTTTTCTTT CTTTTTCTTA AGAAATAAAC GAACGTAGAT TGCGGCTCAA 2100
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2140

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Theobroma cacao
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Val Ile Ser Lys Ser Pro Phe Ile Val Leu Ile Phe Ser Leu Leu
 1 5 10 15
 45 Leu Ser Phe Ala Leu Leu Cys Ser Gly Val Ser Ala Tyr Gly Arg Lys
 20 25 30
 Gln Tyr Glu Arg Asp Pro Arg Gln Gln Tyr Glu Gln Cys Gln Arg Arg
 35 40 45
 50 Cys Glu Ser Glu Ala Thr Glu Glu Arg Glu Gln Glu Gln Cys Glu Gln
 50 55 60
 55 Arg Cys Glu Arg Glu Tyr Lys Glu Gln Gln Arg Gln Gln Glu Glu Glu
 65 70 75 80

48

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Leu | Gln | Arg | Gln | Tyr | Gln | Gln | Cys | Gln | Gly | Arg | Cys | Gln | Glu | Gln | Gln | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| 5 | Gln | Gly | Gln | Arg | Glu | Gln | Gln | Gln | Cys | Gln | Arg | Lys | Cys | Trp | Glu | Gln | |
| | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Tyr | Lys | Glu | Gln | Glu | Arg | Gly | Glu | His | Glu | Asn | Tyr | His | Asn | His | Lys | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 10 | Lys | Asn | Arg | Ser | Glu | Glu | Glu | Glu | Gly | Gln | Gln | Arg | Asn | Asn | Pro | Tyr | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Tyr | Phe | Pro | Lys | Arg | Arg | Ser | Phe | Gln | Thr | Arg | Phe | Arg | Asp | Glu | Glu | |
| 15 | | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| | Gly | Asn | Phe | Lys | Ile | Leu | Gln | Arg | Phe | Ala | Glu | Asn | Ser | Pro | Pro | Leu | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 20 | Lys | Gly | Ile | Asn | Asp | Tyr | Arg | Leu | Ala | Met | Phe | Glu | Ala | Asn | Pro | Asn | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Thr | Phe | Ile | Leu | Pro | His | His | Cys | Asp | Ala | Glu | Ala | Ile | Tyr | Phe | Val | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 25 | Thr | Asn | Gly | Lys | Gly | Thr | Ile | Thr | Phe | Val | Thr | His | Glu | Asn | Lys | Glu | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Ser | Tyr | Asn | Val | Gln | Arg | Gly | Thr | Val | Val | Ser | Val | Pro | Ala | Gly | Ser | |
| 30 | | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| | Thr | Val | Tyr | Val | Val | Ser | Gln | Asp | Asn | Gln | Glu | Lys | Leu | Thr | Ile | Ala | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 35 | Val | Leu | Ala | Leu | Pro | Val | Asn | Ser | Pro | Gly | Lys | Tyr | Glu | Leu | Phe | Phe | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | Pro | Ala | Gly | Asn | Asn | Lys | Pro | Glu | Ser | Tyr | Tyr | Gly | Ala | Phe | Ser | Tyr | |
| | | | 275 | | | | 280 | | | | | | 285 | | | | |
| 40 | Glu | Val | Leu | Glu | Thr | Val | Phe | Asn | Thr | Gln | Arg | Glu | Lys | Leu | Glu | Glu | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | Ile | Leu | Glu | Glu | Gln | Arg | Gly | Gln | Lys | Arg | Gln | Gln | Gly | Gln | Gln | Gly | |
| 45 | | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| | Met | Phe | Arg | Lys | Ala | Lys | Pro | Glu | Gln | Ile | Arg | Ala | Ile | Ser | Gln | Gln | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 50 | Ala | Thr | Ser | Pro | Arg | His | Arg | Gly | Gly | Glu | Arg | Leu | Ala | Ile | Asn | Leu | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| | Leu | Ser | Gln | Ser | Pro | Val | Tyr | Ser | Asn | Gln | Asn | Gly | Arg | Phe | Phe | Glu | |
| | | | 355 | | | | | 360 | | | | 365 | | | | | |
| 55 | Ala | Cys | Pro | Glu | Asp | Phe | Ser | Gln | Phe | Gln | Asn | Met | Asp | Val | Ala | Val | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |

Ser Ala Phe Lys Leu Asn Gln Gly Ala Ile Phe Val Pro His Tyr Asn
 385 390 395 400
 5 Ser Lys Ala Thr Phe Val Val Phe Val Thr Asp Gly Tyr Gly Tyr Ala
 405 410 415
 Gln Met Ala Cys Pro His Leu Ser Arg Gln Ser Gln Gly Ser Gln Ser
 420 425 430
 10 Gly Arg Gln Asp Arg Arg Glu Gln Glu Glu Glu Ser Glu Glu Glu Thr
 435 440 445
 Phe Gly Glu Phe Gln Gln Val Lys Ala Pro Leu Ser Pro Gly Asp Val
 450 455 460
 15 Phe Val Ala Pro Ala Gly His Ala Val Thr Phe Phe Ala Ser Lys Asp
 465 470 475 480
 20 Gln Pro Leu Asn Ala Val Ala Phe Gly Leu Asn Ala Gln Asn Asn Gln
 485 490 495
 Arg Ile Phe Leu Ala Gly Arg Pro Phe Phe Leu Asn His Lys Gln Asn
 500 505 510
 25 Thr Asn Val Ile Lys Phe Thr Val Lys Ala Ser Ala Tyr
 515 520 525
 30 (2) INFORMATION FOR SEQ ID NO: 8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 amino acids
 (B) TYPE: amino acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Gossypium hirsutum*
 (F) TISSUE TYPE: Seeds
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 Met Val Arg Asn Lys Ser Ala Cys Val Val Leu Leu Phe Ser Leu Phe
 1 5 10 15
 Leu Ser Phe Gly Leu Leu Cys Ser Ala Lys Asp Phe Pro Gly Arg Arg
 20 25 30
 Gly Asp Asp Asp Pro Pro Lys Arg Tyr Glu Asp Cys Arg Arg Arg Cys
 35 40 45
 55 Glu Trp Asp Thr Arg Gly Gln Lys Glu Gln Gln Gln Cys Glu Glu Ser
 50 55 60

Cys Lys Ser Gln Tyr Gly Glu Lys Asp Gln Gln Gln Arg His Arg Pro
 65 70 75 80
 5 Glu Asp Pro Gln Arg Arg Tyr Glu Glu Cys Gln Gln Glu Cys Arg Gln
 85 90 95
 Gln Glu Glu Arg Gln Gln Pro Gln Cys Gln Gln Arg Cys Leu Lys Arg
 100 105 110
 10 Phe Glu Gln Glu Gln Gln Gln Ser Gln Arg Gln Phe Gln Glu Cys Gln
 115 120 125
 Gln His Cys His Gln Gln Glu Gln Arg Pro Glu Lys Lys Gln Gln Cys
 130 135 140
 15 Val Arg Glu Cys Arg Glu Lys Tyr Gln Glu Asn Pro Trp Arg Gly Glu
 145 150 155 160
 20 Arg Glu Glu Glu Ala Glu Glu Glu Glu Thr Glu Glu Gly Glu Gln Glu
 165 170 175
 Gln Ser His Asn Pro Phe His Phe His Arg Arg Ser Phe Gln Ser Arg
 180 185 190
 25 Phe Arg Glu Glu His Gly Asn Phe Arg Val Leu Gln Arg Phe Ala Ser
 195 200 205
 Arg His Pro Ile Leu Arg Gly Ile Asn Glu Phe Arg Leu Ser Ile Leu
 210 215 220
 Glu Ala Asn Pro Asn Thr Phe Val Leu Pro His His Cys Asp Ala Glu
 225 230 235 240
 35 Lys Ile Tyr Leu Val Thr Asn Gly Arg Gly Thr Leu Thr Phe Leu Thr
 245 250 255
 His Glu Asn Lys Glu Ser Tyr Asn Ile Val Pro Gly Val Val Val Lys
 260 265 270
 40 Val Pro Ala Gly Ser Thr Val Tyr Leu Ala Asn Gln Asp Asn Lys Glu
 275 280 285
 Lys Leu Ile Ile Ala Val Leu His Arg Pro Val Asn Asn Pro Gly Gln
 290 295 300
 Phe Glu Glu Phe Phe Pro Ala Gly Ser Gln Arg Pro Gln Ser Tyr Leu
 305 310 315 320
 50 Arg Ala Phe Ser Arg Glu Ile Leu Glu Pro Ala Phe Asn Thr Arg Ser
 325 330 335
 Glu Gln Leu Asp Glu Leu Phe Gly Gly Arg Gln Ser Arg Arg Arg Gln
 340 345 350
 55 Gln Gly Gln Gly Met Phe Arg Lys Ala Ser Gln Glu Gln Ile Arg Ala

51

355

360

365

5 Leu Ser Gln Glu Ala Thr Ser Pro Arg Glu Lys Ser Gly Glu Arg Phe
 370 375 380
 Ala Phe Asn Leu Leu Ser Gln Thr Pro Arg Tyr Ser Asn Gln Asn Gly
 385 390 395 400
 10 Arg Phe Phe Glu Ala Cys Pro Pro Glu Phe Arg Gln Leu Arg Asp Ile
 405 410 415
 Asn Val Thr Val Ser Ala Leu Gln Leu Asn Gln Gly Ser Ile Phe Val
 420 425 430
 15 Pro His Tyr Asn Ser Lys Ala Thr Phe Val Ile Leu Val Thr Glu Gly
 435 440 445
 Asn Gly Tyr Ala Glu Met Val Ser Pro His Leu Pro Arg Gln Ser Ser
 450 455 460
 20 Tyr Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Gln Glu Gln Glu
 465 470 475 480
 25 Glu Glu Arg Arg Ser Gly Gln Tyr Arg Lys Ile Arg Ser Arg Leu Ser
 485 490 495
 Arg Gly Asp Ile Phe Val Val Pro Ala Asn Phe Pro Val Thr Phe Val
 500 505 510
 30 Ala Ser Gln Asn Gln Asn Leu Arg Met Thr Gly Phe Gly Leu Tyr Asn
 515 520 525
 Gln Asn Ile Asn Pro Asp His Asn Gln Arg Ile Phe Val Ala Gly Lys
 530 535 540
 35 Ile Asn His Val Arg Gln Trp Asp Ser Gln Ala Lys Glu Leu Ala Phe
 545 550 555 560
 40 Gly Val Ser Ser Arg Leu Val Asp Glu Ile Phe Asn Ser Asn Pro Gln
 565 570 575
 Glu Ser Tyr Phe Val Ser Arg Gln Arg Gln Arg Ala Ser Glu
 580 585 590

45 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

52

Arg Gln Arg Asp Pro Gln Gln Gln Ala Glu Gln Ala Gln Lys Arg Ala
1 5 10 15

Gln Arg Arg Glu Thr Glu
20

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Pro Arg His Met Gln Ile Ala Gln Gln Arg Ala Glu Arg Arg Ala Glu
1 5 10 15

Lys Glu Lys Arg Lys Gln Gln Lys Arg
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Ala Trp Phe His Val Ser Val Cys Asn Ala Val Phe Val Val Ile
1 5 10 15

Ile Ile Ile Met Leu Leu Met Phe Val Pro Val Val Arg Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAGCAGCAGT ATGAGCAGTG

20

5 (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTTTTCGTAK CKKCKTTCGC A

21

20 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACACCATATG CGACAACGTG ATCC

24

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGTTGTTTTTC TCTATTCCTA GGGTTG

26

50 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Gly His His His His His His His His His Ser Ser Gly His
1 5 10 15
Ile Glu Gly Arg His Met
20

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

GGGAATTCCA TATGTATGAG CGTGATCCTC GACAGCAATA CGAGCAATGC CAGAGGCGAT 60
GCGAGTCGGA AGCGACTGAA GAAAGGGAGC 90

(2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAAGCGACTG AAGAAAGGGA GCAAGAGCAG TGTGAACAAC GCTGTGAAAG GGAGTACAAG 60
GAGCAGCAGA GACAGCAATA GGGATCCACA C 91

(2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGAATTCCA TATGCTTCAA AGGCAATACC AGCAATGTCA AGGGCGTTGT CAAGAGCAAC 60
 5 AACAGGGGCA GAGAGAGCAG CAGCAGTGCC AGAGAAAATG C 101

(2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

20 GTGTGGATCC CTAGCTCCTA TTTTTTTTGT GATTATGGTA ATTCTCGTGC TCGCCTCTCT 60
 CTTGTTTCCTT ATATTGCTCC CAGCATTTTC TCTGGCACTG CT 102

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Peanut
- (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Arg Gly Arg Val Ser Pro Leu Met Leu Leu Leu Gly Ile Leu Val
 1 5 10 15

45 Leu Ala Ser Val Ser Ala Thr Gln Ala Lys Ser Pro Tyr Arg Lys Thr
 20 25 30

Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln Glu Pro
 35 40 45

50 Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys Leu Glu
 50 55 60

55 Tyr Asp Pro Arg Cys Val Tyr Asp Thr Gly Ala Thr Asn Gln Arg His
 65 70 75 80

Asp Ile Thr Asn Pro Ile Asn Leu Arg Asp Gly Glu Pro Asp Leu Ser
 390 395 400 405
 5 Asn Asn Phe Gly Arg Leu Phe Glu Val Lys Pro Asp Lys Lys Asn Pro
 410 415 420
 Gln Leu Gln Asp Leu Asp Met Met Leu Thr Cys Val Glu Ile Lys Glu
 425 430 435
 10 Gly Ala Leu Met Leu Pro His Phe Asn Ser Lys Ala Met Val Ile Val
 440 445 450
 Val Val Asn Lys Gly Thr Gly Asn Leu Glu Leu Val Ala Val Arg Lys
 455 460 470
 15 Glu Gln Gln Gln Arg Gly Arg Arg Glu Gln Glu Trp Glu Glu Glu Glu
 480 485 490 500
 20 Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu Val Arg Arg Tyr Thr
 505 510 515
 Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met Pro Ala Ala His Pro
 520 525 530
 25 Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu Leu Gly Phe Gly Ile
 535 540 545
 Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala Gly Asp Lys Asp Asn
 550 555 560
 30 Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp Leu Ala Phe Pro Gly
 565 570 575 580
 35 Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn Gln Arg Glu Ser His
 585 590 595
 Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Pro Ser Ser Pro Glu Lys
 600 605 610
 40 Glu Asp Gln Glu Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser
 615 620 625
 45 Ile Leu Lys Ala Phe Asn
 630

(2) INFORMATION FOR SEQ ID NO: 22:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Maize

(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Ser Ala Arg Ile Val Val Leu Leu Ala Thr Leu Leu Cys Ala
 1 5 10 15
 Ala Ala Ala Val Ala Ser Ser Trp Glu Asp Asp Asn His His His His
 20 25 30
 Gly Gly His Lys Ser Gly Gln Cys Val Arg Arg Cys Glu Asp Arg Pro
 35 40 45
 Trp His Gln Arg Pro Arg Cys Leu Glu Gln Cys Arg Glu Glu Glu Arg
 50 55 60
 Glu Lys Arg Gln Glu Arg Ser Arg His Glu Ala Asp Asp Arg Ser Gly
 65 70 75 80
 Glu Gly Ser Ser Glu Asp Glu Arg Glu Gln Glu Lys Glu Lys Gln Lys
 85 90 95
 Asp Arg Arg Pro Tyr Val Phe Asp Arg Arg Ser Phe Arg Arg Val Val
 100 105 110
 Arg Ser Glu Gln Gly Ser Leu Arg Val Leu Arg Pro Phe Asp Glu Val
 115 120 125
 Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Val Leu Glu
 130 135 140
 Ala Asn Pro Arg Ser Phe Val Val Pro Ser His Thr Asp Ala His Cys
 145 150 155 160
 Ile Cys Tyr Val Ala Glu Gly Glu Gly Val Val Thr Thr Ile Glu Asn
 165 170 175 180
 Gly Glu Arg Arg Ser Tyr Thr Ile Lys Gln Gly His Val Phe Val Ala
 185 190 195
 Pro Ala Gly Ala Val Thr Tyr Leu Ala Asn Thr Asp Gly Arg Lys Lys
 200 205 210
 Leu Val Ile Thr Lys Ile Leu His Thr Ile Ser Val Pro Gly Glu Phe
 215 220 225
 Gln Phe Phe Phe Gly Pro Gly Gly Arg Asn Pro Glu Ser Phe Leu Ser
 230 235 240 245
 Ser Phe Ser Lys Ser Ile Gln Arg Ala Ala Tyr Lys Thr Ser Ser Asp
 250 255 260
 Arg Leu Glu Arg Leu Phe Gly Arg His Gly Gln Asp Lys Gly Ile Ile

[illegible]

Met Val Thr Ala Arg Met
5 600

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Maize
(F) TISSUE TYPE: Seeds

Arg Ser Gly Arg Gly Glu Cys Arg Arg Gln Cys Leu Arg Arg His Glu
1 5 10 15

Gly Gln Pro Trp Glu Thr Gln Glu Cys Met Arg Arg Cys Arg Arg Arg
20 25 30

Gly

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Barley
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met Ala Thr Arg Ala Lys Ala Thr Ile Pro Leu Leu Phe Leu Leu Gly
1 5 10 15

Thr Ser Leu Leu Phe Ala Ala Ala Val Ser Ala Ser His Asp Asp Glu
20 25 30

55 Asp Asp Arg Arg Gly Gly His Ser Leu Gln Gln Cys Val Gln Arg Cys
 35 40 45

Arg Gln Glu Arg Pro Arg Tyr Ser His Ala Arg Cys Val Gln Glu Cys
 50 55 60

5 Arg Asp Asp Gln Gln Gln His Gly Arg His Glu Gln Glu Glu Gln
 65 70 75 80

Gly Arg Gly Arg Gly Trp His Gly Glu Gly Glu Arg Glu Glu Glu His
 85 90 95

10 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu His
 100 105 110

15 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
 115 120 125

Gly Arg Gly His Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Arg
 130 135 140

20 Gly Arg Gly Arg Gly Arg His Gly Glu Gly Glu Arg Glu Glu Glu Glu
 145 150 155 160

Gly Arg Gly Arg Gly Arg Arg Gly Glu Gly Glu Arg Asp Glu Glu Gln
 165 170 175 180

25 Gly Asp Ser Arg Arg Pro Tyr Val Phe Gly Pro Arg Ser Phe Arg Arg
 185 190 195

30 Ile Ile Gln Ser Asp His Gly Phe Val Arg Ala Leu Arg Pro Phe Asp
 200 205 210

Gln Val Ser Arg Leu Leu Arg Gly Ile Arg Asp Tyr Arg Val Ala Ile
 215 220 225

35 Met Glu Val Asn Pro Arg Ala Phe Val Val Pro Gly Phe Thr Asp Ala
 230 235 240 245

Asp Gly Val Gly Tyr Val Ala Gln Gly Glu Gly Val Leu Thr Val Ile
 250 255 260

40 Glu Asn Gly Glu Lys Arg Ser Tyr Thr Val Lys Glu Gly Asp Val Ile
 265 270 275

45 Val Ala Pro Ala Gly Ser Ile Met His Leu Ala Asn Thr Asp Gly Arg
 280 285 290

Arg Lys Leu Val Ile Ala Lys Ile Leu His Thr Ile Ser Val Pro Gly
 295 300 305

50 Lys Phe Gln Phe Leu Ser Val Lys Pro Leu Leu Ala Ser Leu Ser Lys
 310 315 320 325

Arg Val Leu Arg Ala Ala Phe Lys Thr Ser Asp Glu Arg Leu Glu Arg
 330 335 340

55 Leu Phe Asn Gln Arg Gln Gly Gln Glu Lys Thr Arg Ser Val Ser Ile

345 350 355
 Val Arg Ala Ser Glu Glu Gln Leu Arg Glu Leu Arg Arg Glu Ala Ala
 360 365 370
 5
 Glu Gly Gly Gln Gly His Arg Trp Pro Leu Pro Pro Phe Arg Gly Asp
 375 380 385
 10
 Ser Arg Asp Thr Phe Asn Leu Leu Glu Gln Arg Pro Lys Ile Ala Asn
 390 395 400 405
 Arg His Gly Arg Leu Tyr Glu Ala Asp Ala Arg Ser Phe His Ala Leu
 410 415 420
 15
 Ala Asn Gln Asp Val Arg Val Ala Val Ala Asn Ile Thr Pro Gly Ser
 425 430 435
 Met Thr Ala Pro Tyr Leu Asn Thr Gln Ser Phe Lys Leu Ala Val Val
 440 445 450
 20
 Leu Glu Gly Glu Gly Glu Val Gln Ile Val Cys Pro His Leu Gly Arg
 455 460 470
 25
 Glu Ser Glu Ser Glu Arg Glu His Gly Lys Gly Arg Arg Arg Glu Glu
 480 485 490 500
 Glu Glu Asp Asp Gln Arg Gln Gln Arg Arg Arg Gly Ser Glu Ser Glu
 505 510 515
 30
 Ser Glu Glu Glu Glu Glu Gln Gln Arg Tyr Glu Thr Val Arg Ala Arg
 520 525 530
 Val Ser Arg Gly Ser Ala Phe Val Val Pro Pro Gly His Pro Val Val
 535 540 545
 35
 Glu Ile Ser Ser Ser Gln Gly Ser Ser Asn Leu Gln Val Val Cys Phe
 550 555 560
 40
 Glu Ile Asn Ala Glu Arg Asn Glu Arg Val Trp Leu Ala Gly Arg Asn
 565 570 575 580
 Asn Val Ile Gly Lys Leu Gly Ser Pro Ala Gln Glu Leu Thr Phe Gly
 585 590 595
 45
 Arg Pro Ala Arg Glu Val Gln Glu Val Phe Arg Ala Gln Asp Gln Asp
 600 605 610
 Glu Gly Phe Val Ala Gly Pro Glu Gln Gln Ser Arg Glu Gln Glu Gln
 615 620 625
 50
 Glu Gln Glu Arg His Arg Arg Arg Gly Asp Arg Gly Arg Gly Asp Glu
 630 635 640
 55
 Ala Val Glu Thr Phe Leu Arg Met Ala Thr Gly Ala Ile
 645 650 655

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Soybean (Glycine max)
 (F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Met Arg Ala Arg Phe Pro Leu Leu Leu Leu Gly Leu Val Phe Leu
1           5           10           15
Ala Ser Val Ser Val Ser Phe Gly Ile Ala Tyr Trp Glu Lys Glu Asn
20          20          25          30
Pro Lys His Asn Lys Cys Leu Gln Ser Cys Asn Ser Glu Arg Asp Ser
25          35          40          45
Tyr Arg Asn Gln Ala Cys His Ala Arg Cys Asn Leu Leu Lys Val Glu
50          55          60
Lys Glu Glu Cys Glu Glu Gly Glu Ile Pro Arg Pro Arg Pro Arg Pro
30          65          70          75          80
Gln His Pro Glu Arg Glu Pro Gln Gln Pro Gly Glu Lys Glu Glu Asp
35          85          90          95
Glu Asp Glu Gln Pro Arg Pro Ile Pro Phe Pro Arg Pro Gln Pro Arg
100         105         110
Gln Glu Glu Glu His Glu Gln Arg Glu Glu Gln Glu Trp Pro Arg Lys
40         115         120         125
Glu Glu Lys Arg Gly Glu Lys Gly Ser Glu Glu Glu Asp Glu Asp Glu
130         135         140
Asp Glu Glu Gln Asp Glu Arg Gln Phe Pro Phe Pro Arg Pro Pro His
45         145         150         155         160
Gln Lys Glu Glu Arg Asn Glu Glu Glu Asp Glu Asp Glu Glu Gln Gln
50         165         170         175         180
Arg Glu Ser Glu Glu Ser Glu Asp Ser Glu Leu Arg Arg His Lys Asn
185         190         195
Lys Asn Pro Phe Leu Phe Gly Ser Asn Arg Phe Glu Thr Leu Phe Lys
55         200         205         210

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| | Asn | Gln | Tyr | Gly | Arg | Ile | Arg | Val | Leu | Gln | Arg | Phe | Asn | Gln | Arg | Ser |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 215 | | | | | | 220 | | | | | 225 | | | | |
| 5 | Pro | Gln | Leu | Gln | Asn | Leu | Arg | Asp | Tyr | Arg | Ile | Leu | Glu | Phe | Asn | Ser |
| | 230 | | | | | 235 | | | | | 240 | | | | | 245 |
| | Lys | Pro | Asn | Thr | Leu | Leu | Leu | Pro | Asn | His | Ala | Asp | Ala | Asp | Tyr | Leu |
| | | | | | 250 | | | | | 255 | | | | | 260 | |
| 10 | Ile | Val | Ile | Leu | Asn | Gly | Thr | Ala | Ile | Leu | Ser | Leu | Val | Asn | Asn | Asp |
| | | | | 265 | | | | | 270 | | | | | 275 | | |
| | Asp | Arg | Asp | Ser | Tyr | Arg | Leu | Gln | Ser | Gly | Asp | Ala | Leu | Arg | Val | Pro |
| | | | 280 | | | | | 285 | | | | | 290 | | | |
| 15 | Ser | Gly | Thr | Thr | Tyr | Tyr | Val | Val | Asn | Pro | Asp | Asn | Asn | Glu | Asn | Leu |
| | | 295 | | | | | 300 | | | | | 305 | | | | |
| 20 | Arg | Leu | Ile | Thr | Leu | Ala | Ile | Pro | Val | Asn | Lys | Pro | Gly | Arg | Phe | Glu |
| | 310 | | | | | 315 | | | | | 320 | | | | | 325 |
| | Ser | Phe | Phe | Leu | Ser | Ser | Thr | Glu | Ala | Gln | Gln | Ser | Tyr | Leu | Gln | Gly |
| | | | | | 330 | | | | | 335 | | | | | 340 | |
| 25 | Phe | Ser | Arg | Asn | Ile | Leu | Glu | Ala | Ser | Tyr | Asp | Thr | Lys | Phe | Glu | Glu |
| | | | | 345 | | | | | 350 | | | | | 355 | | |
| | Ile | Asn | Lys | Val | Leu | Phe | Ser | Arg | Glu | Glu | Gly | Gln | Gln | Gln | Gly | Glu |
| | | | 360 | | | | | 365 | | | | | 370 | | | |
| 30 | Gln | Arg | Leu | Gln | Glu | Ser | Val | Ile | Val | Glu | Ile | Ser | Lys | Glu | Gln | Ile |
| | | 375 | | | | | 380 | | | | | 385 | | | | |
| 35 | Arg | Ala | Leu | Ser | Lys | Arg | Ala | Lys | Ser | Ser | Ser | Arg | Lys | Thr | Ile | Ser |
| | 390 | | | | | 395 | | | | | 400 | | | | | 405 |
| | Ser | Glu | Asp | Lys | Pro | Phe | Asn | Leu | Arg | Ser | Arg | Asp | Pro | Ile | Tyr | Ser |
| | | | | | 410 | | | | | 415 | | | | | 420 | |
| 40 | Asn | Lys | Leu | Gly | Lys | Phe | Phe | Glu | Ile | Thr | Pro | Glu | Lys | Asn | Pro | Gln |
| | | | | 425 | | | | | 430 | | | | | 435 | | |
| | Leu | Arg | Asp | Leu | Asp | Ile | Phe | Leu | Ser | Ile | Val | Asp | Met | Asn | Glu | Gly |
| | | | 440 | | | | | 445 | | | | | 450 | | | |
| 45 | Ala | Leu | Leu | Leu | Pro | His | Phe | Asn | Ser | Lys | Ala | Ile | Val | Ile | Leu | Val |
| | | 455 | | | | | 460 | | | | | 470 | | | | |
| | Ile | Asn | Glu | Gly | Asp | Ala | Asn | Ile | Glu | Leu | Val | Gly | Leu | Lys | Glu | Gln |
| | 480 | | | | | 485 | | | | | 490 | | | | | 500 |
| | Gln | Gln | Glu | Gln | Gln | Gln | Glu | Glu | Gln | Pro | Leu | Glu | Val | Arg | Lys | Tyr |
| | | | | | 505 | | | | | 510 | | | | | 515 | |
| 55 | Arg | Ala | Glu | Leu | Ser | Glu | Gln | Asp | Ile | Phe | Val | Ile | Pro | Ala | Gly | Tyr |
| | | | | 520 | | | | | 525 | | | | | 530 | | |

Pro Val Val Val Asn Ala Thr Ser Asn Leu Asn Phe Phe Ala Ile Gly
535 540 545

5 Ile Asn Ala Glu Asn Asn Gln Arg Asn Phe Leu Ala Gly Ser Gln Asp
550 555 560

Asn Val Ile Ser Gln Ile Pro Ser Gln Val Gln Glu Leu Ala Phe Pro
565 570 575 580

Gly Ser Ala Gln Ala Val Glu Lys Leu Leu Lys Asn Gln Arg Glu Ser
585 590 595

15 Tyr Phe Val Asp Ala Gln Pro Lys Lys Lys Glu Glu Gly Asn Lys Gly
600 605 610

Arg Lys Gly Pro Leu Ser Ser Ile Leu Arg Ala Phe Tyr
615 620 625

20

(2) INFORMATION FOR SEQ ID NO: 26:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26;

Val Lys Glu Asp His Gln Phe Glu Thr Arg Gly Glu Ile Leu Glu Cys
1 5 10 15

40

Tyr Arg Leu Cys Gln Gln Gln
20

45

(28) INFORMATION FOR SEQ ID NO: 27:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

Gln Lys His Arg Ser Gln Ile Leu Gly Cys Tyr Leu Xxx cys Gln Gln
1 5 10 15

Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Stenocarpus sinuatus*
(F) TISSUE TYPE: Seeds

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Leu Asp Pro Ile Arg Gln Gln Gln Leu Cys Gln Met Arg Cys Gln Gln
1 5 10 15

30 Gln Glu Lys Asp Pro Arg Gln Gln Gln Gln Cys Lys
 20 25

[illegible]